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#22

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/455,683

DATE: 08/12/1999  
TIME: 11:32:39

INPUT SET: S32901.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: BELL, GRAEME  
REISINE, TERRY  
YASUDA, KAZUKI

(ii) TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold, White & Durkee  
(B) STREET: P. O. Box 4433  
(C) CITY: Houston  
(D) STATE: Texas  
(E) COUNTRY: USA  
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/455,683  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/292,694  
(B) FILING DATE:  
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: 08/100,694  
(B) FILING DATE: 30 July, 1993  
(C) CLASSIFICATION: Unknown

(A) APPLICATION NUMBER: 08/147,592  
(B) FILING DATE: 5 November 1993  
(C) CLASSIFICATION: Unknown

(A) APPLICATION NUMBER: PCT/US94/05747  
(B) FILING DATE: 20 May 1994

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47      (C) CLASSIFICATION: Unknown
48
49      (viii) ATTORNEY/AGENT INFORMATION:
50          (A) NAME: MARK B. WILSON
51          (B) REGISTRATION NUMBER: 37,259
52          (C) REFERENCE/DOCKET NUMBER: ARCD:140/WIM
53
54      (ix) TELECOMMUNICATION INFORMATION:
55          (A) TELEPHONE: (512) 418-3000
56          (B) TELEFAX: (713) 789-2679
57          (C) TELEX: 79-0924
58
59
60      (2) INFORMATION FOR SEQ ID NO:1:
61
62          (i) SEQUENCE CHARACTERISTICS:
63              (A) LENGTH: 1410 base pairs
64              (B) TYPE: nucleic acid
65              (C) STRANDEDNESS: single
66              (D) TOPOLOGY: linear
67
68          (ii) MOLECULE TYPE: genomic DNA
69
70          (ix) FEATURE:
71              (A) NAME/KEY: CDS
72              (B) LOCATION: 186..1325
73          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
74
75      GCGCACCTTG CTGATCCCAA ACAGGCAGAG CTTCTTCCAG TCTTGAAGG CACAAATTGA      60
76
77      GCATCAGGAA CGTGGACCCA TCAGGGCTGA ACAGCTACTC AGGATCTAAA GTGGTGACTT      120
78
79      GGAAAGCTGA CGGTGACTTG GGAAGGGAGG TCGCCAATCA GCGATCTGGA GCTGCAGCGC      180
80
81      TCACC ATG GAG TCC CCC ATT CAG ATC TTC CGA GGA GAT CCA GGC CCT      227
82      Met Glu Ser Pro Ile Gln Ile Phe Arg Gly Asp Pro Gly Pro
83      1          5          10
84
85      ACC TGC TCT CCC AGT GCT TGC CTT CTC CCC AAC AGC AGC TCT TGG TTC      275
86      Thr Cys Ser Pro Ser Ala Cys Leu Leu Pro Asn Ser Ser Ser Trp Phe
87      15          20          25          30
88
89      CCC AAC TGG GCA GAA TCC GAC AGT AAT GGC AGT GTG GGC TCA GAG GAT      323
90      Pro Asn Trp Ala Glu Ser Asp Ser Asn Gly Ser Val Gly Ser Glu Asp
91      35          40          45
92
93      CAG CAG CTG GAG TCC GCG CAC ATC TCT CCG GCC ATC CCT GTT ATC ATC      371
94      Gln Gln Leu Glu Ser Ala His Ile Ser Pro Ala Ile Pro Val Ile Ile
95      50          55          60
96
97      ACC GCT GTC TAC TCT GTG GTA TTT GTG GTG GGC TTA GTG GGC AAT TCT      419
98      Thr Ala Val Tyr Ser Val Val Phe Val Val Gly Leu Val Gly Asn Ser
99      65          70          75

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100	INPUT SET: S32901.raw																
101	CTG	GTC	ATG	TTT	GTC	ATC	ATC	CGA	TAC	ACG	AAG	ATG	AAG	ACC	GCA	ACC	467
102	Leu	Val	Met	Phe	Val	Ile	Ile	Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	
103	80						85			90							
104																	
105	AAC	ATC	TAC	ATA	TTT	AAC	CTG	GCT	TTG	GCA	GAT	GCT	TTG	GTT	ACT	ACC	515
106	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Val	Thr	Thr	
107	95			100			105			110							
108																	
109	ACT	ATG	CCC	TTT	CAG	AGT	GCT	GTC	TAC	TTG	ATG	AAT	TCT	TGG	CCT	TTT	563
110	Thr	Met	Pro	Phe	Gln	Ser	Ala	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	
111				115			120			125							
112																	
113	GGA	GAT	GTG	CTA	TGC	AAG	ATT	GTC	ATT	TCC	ATT	GAC	TAC	TAC	AAC	ATG	611
114	Gly	Asp	Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	
115				130			135			140							
116																	
117	TTT	ACC	AGC	ATA	TTC	ACC	TTG	ACC	ATG	ATG	AGT	GTG	GAC	CGC	TAC	ATT	659
118	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	
119	145						150			155							
120																	
121	GCT	GTG	TGC	CAC	CCT	GTG	AAA	GCT	TTG	GAC	TTC	CGA	ACA	CCT	TTG	AAA	707
122	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	
123	160						165			170							
124																	
125	GCA	AAG	ATC	ATC	AAC	ATC	TGC	ATT	TGG	CTC	CTG	GCA	TCA	TCT	GTT	GGT	755
126	Ala	Lys	Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ala	Ser	Ser	Val	Gly	
127	175			180			185			190							
128																	
129	ATA	TCA	GCG	ATA	GTC	CTT	GGA	GGC	ACC	AAA	GTC	AGG	GAA	GAT	GTG	GAT	803
130	Ile	Ser	Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Asp	
131				195			200			205							
132																	
133	GTC	ATT	GAA	TGC	TCC	TTG	CAG	TTT	CCT	GAT	GAT	GAA	TAT	TCC	TGG	TGG	851
134	Val	Ile	Glu	Cys	Ser	Leu	Gln	Phe	Pro	Asp	Asp	Glu	Tyr	Ser	Trp	Trp	
135				210			215			220							
136																	
137	GAT	CTC	TTC	ATG	AAG	ATC	TGT	GTC	TTC	GTC	TTT	GCC	TTT	GTG	ATC	CCA	899
138	Asp	Leu	Phe	Met	Lys	Ile	Cys	Val	Phe	Val	Phe	Ala	Phe	Val	Ile	Pro	
139	225						230			235							
140																	
141	GTC	CTC	ATC	ATC	ATT	GTC	TGC	TAC	ACC	CTG	ATG	ATC	CTG	CGC	CTG	AAG	947
142	Val	Leu	Ile	Ile	Ile	Val	Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	
143	240						245			250							
144																	
145	AGT	GTC	CGG	CTC	CTG	TCT	GGC	TCC	CGA	GAG	AAG	GAC	CGA	AAT	CTC	CGC	995
146	Ser	Val	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	
147	255			260			265			270							
148																	
149	CGC	ATC	ACC	AAG	CTG	GTG	CTG	GTA	GTA	GTT	GCA	GTC	TTC	ATC	ATC	TGT	1043
150	Arg	Ile	Thr	Lys	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Ile	Cys	
151																	

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153   TGG ACC CCC ATT CAC ATC TTT ATC CTG GTG GAG GCT CTG GGA AGC ACC      1091
154   Trp Thr Pro Ile His Ile Phe Ile Leu Val Glu Ala Leu Gly Ser Thr
155               290                      295                      300
156
157   TCC CAC AGC ACA GCT GCC CTC TCC AGC TAT TAT TTC TGT ATT GCC TTG      1139
158   Ser His Ser Thr Ala Ala Leu Ser Ser Tyr Tyr Phe Cys Ile Ala Leu
159               305                      310                      315
160
161   GGT TAT ACC AAC AGC AGC CTG AAT CCT GTT CTC TAT GCC TTT CTG GAT      1187
162   Gly Tyr Thr Asn Ser Ser Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp
163               320                      325                      330
164
165   GAA AAC TTC AAG CGG TGT TTT AGG GAC TTC TGC TTC CCT ATT AAG ATG      1235
166   Glu Asn Phe Lys Arg Cys Phe Arg Asp Phe Cys Phe Pro Ile Lys Met
167   335                      340                      345                      350
168
169   CGA ATG GAG CGC CAG AGC ACC AAT AGA GTT AGA AAC ACA GTT CAG GAT      1283
170   Arg Met Glu Arg Gln Ser Thr Asn Arg Val Arg Asn Thr Val Gln Asp
171               355                      360                      365
172
173   CCT GCT TCC ATG AGA GAT GTG GGA GGG ATG AAT AAG CCA GTA      1325
174   Pro Ala Ser Met Arg Asp Val Gly Gly Met Asn Lys Pro Val
175               370                      375                      380
176
177   TGACTAGTCG TGGAAATGTC TTCTTATTGT TCTCCAGGTA GAGAAGAGTT CAATGATCTT      1385
178
179   GGTTTAACCC AGATTACAAC TGCAG      1410
180
181
182   (2) INFORMATION FOR SEQ ID NO:2:
183
184       (i) SEQUENCE CHARACTERISTICS:
185           (A) LENGTH: 380 amino acids
186           (B) TYPE: amino acid
187           (D) TOPOLOGY: linear
188
189       (ii) MOLECULE TYPE: protein

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